



TABLE 1: Genes Included in the Application

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXA01524	GR00424	29041	30483	Lincomycin RESISTANCE PROTEIN
3	4	RXA00497	GR00124	52	348	10 KD CHAPERONIN
5	6	RXN00493	VV0086	14389	16002	60 KD CHAPERONIN
7	8	F RXA00498	GR00124	363	1601	60 KD CHAPERONIN
9	10	RXA01217	GR00353	802	203	GENERAL STRESS PROTEIN CTC
11	12	RXA00605	GR00159	7412	5865	CATALASE (EC 1.11.1.6)
13	14	RXA00404	GR00089	2909	594	CARBON STARVATION PROTEIN A
15	16	RXN03119	VV0098	86877	87008	SUPEROXIDE DISMUTASE (MN) (EC 1.15.1.1)
17	18	RXN03120	VV0098	87351	87476	SUPEROXIDE DISMUTASE (MN) (EC 1.15.1.1)
19	20	RXN00575	VV0323	14716	15252	PHOSPHOTHIOICIN-RESISTANCE PROTEIN
21	22	F RXA00575	GR00156	2130	1648	PHOSPHOTHIOICIN-RESISTANCE PROTEIN

Chaperones

<u>Nucleic Acid</u> <u>SEQ ID NO</u>	<u>Amino Acid</u> <u>SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
23	24	RXN01345	VV0123	4883	3432	Molecular chaperon (HSP70/Dnak family)
25	26	F RXA01345	GR00391	1172	6	Molecular chaperones (HSP70/Dnak family)
27	28	RXA02541	GR00726	13657	12473	DNAJ PROTEIN
29	30	RXA02542	GR00726	14518	13865	GRPE PROTEIN
31	32	RXN02543	VV0057	22031	20178	DNAK PROTEIN
33	34	F RXA02543	GR00726	16375	14522	DNAK PROTEIN
35	36	RXN02280	VV0152	1849	26	TRAP1
37	38	F RXA02282	GR00659	1145	1480	Molecular chaperone, HSP90 family
39	40	RXA00886	GR00242	12396	13541	DNAJ PROTEIN
41	42	RXS00568	VV0251	2928	1582	TRIGGER FACTOR
43	44	RXN03038	VV0017	42941	43666	PS1 PROTEIN VORLAUFER
45	46	RXN03039	VV0018	2	631	PS1 PROTEIN VORLAUFER
47	48	RXN03040	VV0018	761	1069	PS1 PROTEIN VORLAUFER
49	50	RXN03051	VV0022	2832	3566	PS1 PROTEIN VORLAUFER
51	52	RXN03054	VV0026	1906	3486	PS1 PROTEIN VORLAUFER
53	54	RXN02949	VV0025	31243	31755	PREPROTEIN TRANSLOKASE SECE UNTEREINHEIT
55	56	RXN02462	VV0124	11932	13749	PREPROTEIN TRANSLOKASE SECA UNTEREINHEIT
57	58	RXN01559	VV0171	7795	5954	PROTEIN-EXPORT MEMBRANE PROTEIN SECD
59	60	RXN00046	VV0119	5363	6058	Signal Erkennung particle GTPase
61	62	RXN01863	VV0206	1172	24	/O/C Thioedoxin-ähnliche oxido-reductase
63	64	RXN00833	VV0180	8039	8533	THIOL PEROXIDASE (EC 1.11.1.-)

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65	66	RXN01676	VW0179	12059	11304	THIOL-DISULFIDE AUSTAUSCH PROTEIN DSB
67	68	RXN00380	VW0223	836	216	THIOL-DISULFIDE AUSTAUSCH PROTEIN TLP
69	70	RXN00937	VW0079	42335	42706	THIOREDOXIN
71	72	RXN02325	VW0047	5527	6393	THIOREDOXIN
73	74	RXN01837	VW0320	7103	7879	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8)
75	76	RXN01926	VW0284	1	741	PEPTID KETTE RELEASE FACTOR 3
77	78	RXN02002	VW0111	141	518	PEPTID KETTE RELEASE FACTOR 3
79	80	RXN02736	VW0074	13600	14556	PUTATIVES OXPRCYCLE PROTEIN OPCA
81	82	RXS03217				SMALL COLD-SHOCK PROTEIN
83	84	F RXA01917	GR00549	3465	3665	SMALL COLD-SHOCK PROTEIN

Proteins involved in stress responses

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
85	86	RXA02184	GR00641	19628	19248	COLD SHOCK-LIKE PROTEIN CSPC
87	88	RXA00810	GR00218	792	992	SMALL COLD-SHOCK PROTEIN
89	90	RXA01674	GR00467	1878	2771	PROBABLE HYDROGEN PEROXIDE-INDUCIBLE GENES ACTIVATOR
91	92	RXA02431	GR00708	2	1192	damage-inducible protein P
93	94	RXA02446	GR00709	11640	11206	OSMOTICALLY INDUCIBLE PROTEIN C
95	96	RXA02861	GR10006	551	1633	probable metallothionein u0308aa - Mycobacterium leprae
97	98	RXA00981	GR00276	3388	4017	GTP PYROPHOSPHOKINASE (EC 2.7.6.5)
99	100	RXN00786	VW0321	1680	706	LYTB PROTEIN
101	102	RXS01027	VW0143	5761	6768	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
103	104	RXS01528	VW0050	17276	16749	DIADENOSINE 5',5''-P ₁ ,P ₄ -TETRAPHOSPHATE HYDROLASE (EC 3.6.1.17)
105	106	RXS01716	VW0319	3259	2774	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
107	108	RXS01835	VW0143	10575	10045	GUANOSINE-3',5'-BIS(DIPHOSPHATE) 3'-PYROPHOSPHOHYDROLASE (EC 3.1.7.2)
109	110	RXS02497	VW0007	15609	16535	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
111	112	RXS02972	VW0319	2763	2353	EXOPOLYPHOSPHATASE (EC 3.6.1.11)

Resistance and tolerance

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
113	114	RXA02159	GR00640	6231	6743	ARGININE HYDROXIMATE RESISTANCE PROTEIN
115	116	RXA02201	GR00646	5837	6199	ARSENATE REDUCTASE
117	118	RXA00599	GR00159	1843	1457	ARSENICAL-RESISTANCE PROTEIN ACRA3
119	120	RXA00600	GR00159	2940	1843	ARSENICAL-RESISTANCE PROTEIN ACRA3
121	122	RXA02200	GR00646	4651	5760	ARSENICAL-RESISTANCE PROTEIN ACRA3
123	124	RXA02202	GR00646	6278	6916	ARSENICAL-RESISTANCE PROTEIN ACRA3
125	126	RXA02205	GR00646	9871	8993	BACITRACIN RESISTANCE PROTEIN (PUTATIVE UNDECAPRENOL KINASE) (EC 2.7.1.66)
127	128	RXA00900	GR00245	4052	3201	BICYCLOWYCIN RESISTANCE PROTEIN

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129	130	RXN00901	VV0140	8561	8168	BICYCLOMYCIN RESISTANCE PROTEIN
131	132	F RXA00901	GR00245	4337	3980	BICYCLOMYCIN RESISTANCE PROTEIN
133	134	RXA00289	GR00046	3263	4438	CHLORAMPHENICOL RESISTANCE PROTEIN
135	136	RXN01984	VV0056	1515	1811	CHLORAMPHENICOL RESISTANCE PROTEIN
137	138	F RXA01984	GR00574	282	4	CHLORAMPHENICOL RESISTANCE PROTEIN
139	140	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
141	142	RXA00109	GR00015	1176	565	COPPER RESISTANCE PROTEIN C PRECURSOR
143	144	RXA00996	GR00283	1763	1023	DAUNORUBICIN RESISTANCE ATP-BINDING PROTEIN DRRA
145	146	RXN00829	VV0180	7950	5611	DAUNORUBICIN RESISTANCE PROTEIN
147	148	F RXA00829	GR00224	2	256	DAUNORUBICIN RESISTANCE PROTEIN
149	150	F RXA00834	GR00225	463	2025	DAUNORUBICIN RESISTANCE PROTEIN
151	152	RXA00995	GR00283	1023	283	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
153	154	RXN00803	VV0009	53658	52629	METHYLENOMYCIN A RESISTANCE PROTEIN
155	156	F RXA00803	GR00214	4560	5162	METHYLENOMYCIN A RESISTANCE PROTEIN
157	158	RXA01407	GR00410	3918	3028	METHYLENOMYCIN A RESISTANCE PROTEIN
159	160	RXA01408	GR00410	4384	4184	METHYLENOMYCIN A RESISTANCE PROTEIN
161	162	RXN01922	VV0020	2031	3182	METHYLENOMYCIN A RESISTANCE PROTEIN
163	164	F RXA01922	GR00552	1	1109	METHYLENOMYCIN A RESISTANCE PROTEIN
165	166	RXA02060	GR00626	3	339	MYCINAMICIN-RESISTANCE PROTEIN MYRA
167	168	RXN01936	VV0127	40116	41387	MACROLIDE-EFFLUX PROTEIN
169	170	F RXA01936	GR00555	9796	8975	NICKEL RESISTANCE PROTEIN
171	172	F RXA01937	GR00555	10246	9821	NICKEL RESISTANCE PROTEIN
173	174	RXN01010	VV0209	3776	4894	QUINOLONE RESISTANCE NORA PROTEIN
175	176	F RXA01010	GR00288	774	4	QUINOLONE RESISTANCE NORA PROTEIN
177	178	RXN03142	VV0136	5754	4612	QUINOLONE RESISTANCE NORA PROTEIN
179	180	F RXA01150	GR00323	3807	2917	QUINOLONE RESISTANCE NORA PROTEIN
181	182	RXN02964	VV0102	7931	6714	QUINOLONE RESISTANCE NORA PROTEIN
183	184	F RXA02116	GR00636	911	6	QUINOLONE RESISTANCE NORA PROTEIN
185	186	RXA00858	GR00233	1660	2147	TELLURIUM RESISTANCE PROTEIN TERC
187	188	RXA02305	GR00663	2921	2070	DAUNOMYCIN C-14 HYDROXYLASE
189	190	RXA00084	GR00013	2367	1543	VIBRIOBACTIN UTILIZATION PROTEIN VVIB
191	192	RXA00843	GR00228	3236	3580	ARSENATE REDUCTASE
193	194	RXA01052	GR00296	3398	3706	MERCURIC REDUCTASE (EC 1.16.1.1)
195	196	RXA01053	GR00296	3772	4191	MERCURIC REDUCTASE (EC 1.16.1.1)
197	198	RXA01054	GR00296	4229	4717	MERCURIC REDUCTASE (EC 1.16.1.1)
199	200	RXN03123	VV0106	808	1245	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
201	202	F RXA00993	GR00282	641	6	HEAVY METAL TOLERANCE PROTEIN PRECURSOR
203	204	RXA01051	GR00296	3298	2690	VANZ PROTEIN, leicoplanin resistance protein
205	206	RXN01873	VV0248	2054	819	Hypothetical Drug Resistance Protein
207	208	F RXA01873	GR00535	855	1946	Hypothetical Drug Resistance Protein
209	210	RXN00034	VV0020	16933	18381	MULTIDRUG RESISTANCE PROTEIN B
211	212	F RXA02273	GR00655	8058	9002	Hypothetical Drug Resistance Protein
213	214	RXN03075	VV0042	2491	3216	Hypothetical Drug Transporter
215	216	F RXA02907	GR10044	1395	2120	Hypothetical Drug Transporter
217	218	RXA00479	GR00119	16290	14101	Hypothetical Drug Transporter
219	220	RXN03124	VV0108	4	963	Hypothetical Drug Transporter
221	222	F RXA01180	GR00336	4	765	Hypothetical Drug Transporter

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223	224	RXA02586	GR00741	10296	10027	Hypothetical Drug Transporter
225	226	RXA02587	GR00741	12343	10253	Hypothetical Drug Transporter
227	228	RXN03042	VV0018	2440	1835	Hypothetical Drug Transporter
229	230	F RXA02893	GR10035	1841	1236	MULTIDRUG EFFLUX PROTEIN OACB
231	232	RXA01616	GR00450	1684	203	MULTIDRUG RESISTANCE PROTEIN
233	234	RXA01666	GR00463	2307	3683	MULTIDRUG RESISTANCE PROTEIN B
235	236	RXA00062	GR00009	13252	11855	MULTIDRUG RESISTANCE PROTEIN B
237	238	RXA00215	GR00032	13834	15294	MULTIDRUG RESISTANCE PROTEIN B
239	240	RXN03064	VV0038	4892	6223	MULTIDRUG RESISTANCE PROTEIN B
241	242	F RXA00565	GR00151	4892	5884	MULTIDRUG RESISTANCE PROTEIN B
243	244	F RXA02878	GR10016	1837	1481	MULTIDRUG RESISTANCE PROTEIN B
245	246	RXA00648	GR00169	2713	1304	MULTIDRUG RESISTANCE PROTEIN B
247	248	RXN01320	VV0082	13146	11500	MULTIDRUG RESISTANCE PROTEIN B
249	250	F RXA01314	GR00382	744	4	MULTIDRUG RESISTANCE PROTEIN B
251	252	F RXA01320	GR00383	1979	1200	MULTIDRUG RESISTANCE PROTEIN B
253	254	RXN02926	VV0082	11497	9866	MULTIDRUG RESISTANCE PROTEIN B
255	256	F RXA01319	GR00383	1197	4	MULTIDRUG RESISTANCE PROTEIN B
257	258	RXA01578	GR00439	1423	29	MULTIDRUG RESISTANCE PROTEIN B
259	260	RXA02087	GR00629	7076	5730	MULTIDRUG RESISTANCE PROTEIN B
261	262	RXA02088	GR00629	8294	7080	MULTIDRUG RESISTANCE PROTEIN B
263	264	RXA00764	GR00204	3284	2169	MULTIDRUG RESISTANCE PROTEIN B
265	266	RXN03125	VV0108	972	1142	Hypothetical Drug Transporter
267	268	RXN01553	VV0135	25201	26520	Hypothetical Drug Permease
269	270	RXN00535	VV0219	5155	5871	Hypothetical Drug Resistance Protein
271	272	RXN00453	VV0076	1173	3521	Hypothetical Drug Transporter
273	274	RXN00932	VV0171	13120	13593	Hypothetical Drug Transporter
275	276	RXN03022	VV0002	65	511	MULTIDRUG RESISTANCE PROTEIN B
277	278	RXN03151	VV0163	489	4	MYCINAMICIN-RESISTANCE PROTEIN MYRA
279	280	RXN02832	VV0358	547	5	LYSOSTAPHIN IMMUNITY FACTOR
281	282	RXN00165	VV0232	3275	1860	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
283	284	RXN01190	VV0169	8992	10338	MULTIDRUG RESISTANCE-LIKE ATP-BINDING PROTEIN MDL
285	286	RXN01102	VV0059	6128	4884	QUINOLONE RESISTANCE NORA PROTEIN
287	288	RXN00788	VV0321	3424	3648	CHLORAMPHENICOL RESISTANCE PROTEIN
289	290	RXN02119	VV0102	11242	9602	AZ01A-RESISTANCE ATP-BINDING PROTEIN
291	292	RXN01605	VV0137	7124	5610	DAUNORUBICIN RESISTANCE TRANSMEMBRANE PROTEIN
293	294	RXN01091	VV0326	567	4	MAZG PROTEIN
295	296	RXS02979	VV0149	2150	2383	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
297	298	RXS02987	VV0234	527	294	MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT PRECURSOR
299	300	RXS03095	VV0057	4056	4424	CADMIUM EFFLUX SYSTEM ACCESSORY PROTEIN HOMOLOG

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	dsr		Kimura, E. et al. "Molecular cloning of a novel gene, dsrR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	dsrI; dsrR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dcIAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the <i>Corynebacterium glutamicum</i> rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in <i>Corynebacterium glutamicum</i> ," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	pand	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the <i>Corynebacterium glutamicum</i> pand gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in <i>Escherichia coli</i> ," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD, aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC, aroK, aroB, pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system. ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminiopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc, secG, amt, ocd, soxA	Phosphoenolpyruvate-carboxylase; ?, high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD, srp, amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichter, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the <i>Corynebacterium glutamicum</i> (Brevibacterium lactofermentum AJ12036) <i>odhA</i> gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomerase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomerase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and deshiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

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E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydropyridine reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydropyridine acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydropyridine acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydropyridine acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	ilvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinose 7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of <i>Corynebacterium glutamicum</i> 3-deoxy-D-arabinose 7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	ilvB; ilvN; ilvC	Acetylhydroxy acid synthase large subunit; Acetylhydroxy acid synthase small subunit; Acetylhydroxy acid isomerase	Keilhauer, C. et al. "Isolation and characterization of <i>Corynebacterium glutamicum</i> molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	psm	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dxr from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	aecD; bmQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rossol, I. et al. "The <i>Corynebacterium glutamicum</i> aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminomethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in <i>Corynebacterium glutamicum</i> ATCC 13032 is directed by the bmQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
SS9299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> : identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the <i>Corynebacterium glutamicum</i> ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from <i>Corynebacterium glutamicum</i> ATCC 13032 and analysis of its role in intergeneric conjugation with <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The <i>Corynebacterium glutamicum</i> cglIM gene encoding a 5-cytosine in an McrBC-deficient <i>Escherichia coli</i> strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the <i>Corynebacterium glutamicum</i> proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thtR, accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5'-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Masui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Elkmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum</i> fda gene: structural comparison of C. glutamicum fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambda</i> corynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the <i>Corynebacterium glutamicum</i> lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the <i>Corynebacterium glutamicum</i> trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the <i>Corynebacterium glutamicum</i> threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of <i>Corynebacterium diphtheriae</i> , <i>Corynebacterium ulcerans</i> , <i>Corynebacterium glutamicum</i> , and the attP site of <i>lambda</i> corynephage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kaliowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kaliowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in <i>Corynebacterium glutamicum</i> ," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Elkman, B. J. "Identification, sequence analysis, and expression of a <i>Corynebacterium glutamicum</i> gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerases," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the <i>Corynebacterium glutamicum</i> lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	copI	PSI protein	Joliff, G. et al. "Cloning and nucleotide sequence of the cspI gene encoding PSI, one of the two major secreted proteins of <i>Corynebacterium glutamicum</i> : The deduced N-terminal region of PSI is similar to the <i>Mycobacterium</i> antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Elkmanus, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the <i>Corynebacterium glutamicum</i> gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a <i>Corynebacterium glutamicum</i> IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in <i>Corynebacterium glutamicum</i> : enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Elkmanus, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the <i>Corynebacterium glutamicum</i> icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mttA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of <i>Corynebacterium glutamicum</i> encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of <i>Corynebacterium glutamicum</i> and <i>Brevibacterium lactofermentum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA, thiX	Partial Isocitrate lyase, ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from <i>Corynebacterium glutamicum</i> and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Bilman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> proline reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in <i>Corynebacterium glutamicum</i> : enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the <i>Corynebacterium glutamicum</i> pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE, lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahn, H. et al. "D-pantothenate synthesis in <i>Corynebacterium glutamicum</i> and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer <i>Brevibacterium lactofermentum</i> (<i>Corynebacterium glutamicum</i> ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the <i>Brevibacterium lactofermentum</i> ," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00346	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the <i>Corynebacterium glutamicum</i> hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC;ftsQ/divD;ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from <i>Brevibacterium lactofermentum</i> ," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of <i>Corynebacterium glutamicum</i> proline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from <i>Corynebacterium glutamicum</i> : characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from <i>Corynebacterium glutamicum</i> ," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of coryneophage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS, lysA	Arginyl-tRNA synthetase; diaminiopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA, dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE, dxr	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1, sigB	?, SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CGBS	NCIG	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866								
Brevibacterium	spec.	19240								
Corynebacterium	acetoacidophilum	21476								
Corynebacterium	acetoacidophilum	13870								
Corynebacterium	acetoglutamicum			B11473						
Corynebacterium	acetoglutamicum			B11475						
Corynebacterium	acetoglutamicum	15806								
Corynebacterium	acetoglutamicum	21491								
Corynebacterium	acetoglutamicum	31270								
Corynebacterium	acetophilum			B3671						
Corynebacterium	ammoniagenes	6872						2399		
Corynebacterium	ammoniagenes	15511								
Corynebacterium	fujikense	21496								
Corynebacterium	glutamicum	14067								
Corynebacterium	glutamicum	39137								
Corynebacterium	glutamicum	21254								
Corynebacterium	glutamicum	21255								
Corynebacterium	glutamicum	31830								
Corynebacterium	glutamicum	13032								
Corynebacterium	glutamicum	14305								
Corynebacterium	glutamicum	15455								
Corynebacterium	glutamicum	13058								
Corynebacterium	glutamicum	13059								
Corynebacterium	glutamicum	13060								
Corynebacterium	glutamicum	21492								
Corynebacterium	glutamicum	21513								
Corynebacterium	glutamicum	21526								
Corynebacterium	glutamicum	21543								
Corynebacterium	glutamicum	13287								
Corynebacterium	glutamicum	21851								
Corynebacterium	glutamicum	21253								

Corynebacterium	glutamicum	21514								
Corynebacterium	glutamicum	21516								
Corynebacterium	glutamicum	21299								
Corynebacterium	glutamicum	21300								
Corynebacterium	glutamicum	39684								
Corynebacterium	glutamicum	21488								
Corynebacterium	glutamicum	21649								
Corynebacterium	glutamicum	21650								
Corynebacterium	glutamicum	19223								
Corynebacterium	glutamicum	13869								
Corynebacterium	glutamicum	21157								
Corynebacterium	glutamicum	21158								
Corynebacterium	glutamicum	21159								
Corynebacterium	glutamicum	21355								
Corynebacterium	glutamicum	31808								
Corynebacterium	glutamicum	21674								
Corynebacterium	glutamicum	21562								
Corynebacterium	glutamicum	21563								
Corynebacterium	glutamicum	21564								
Corynebacterium	glutamicum	21565								
Corynebacterium	glutamicum	21566								
Corynebacterium	glutamicum	21567								
Corynebacterium	glutamicum	21568								
Corynebacterium	glutamicum	21569								
Corynebacterium	glutamicum	21570								
Corynebacterium	glutamicum	21571								
Corynebacterium	glutamicum	21572								
Corynebacterium	glutamicum	21573								
Corynebacterium	glutamicum	21579								
Corynebacterium	glutamicum	19049								
Corynebacterium	glutamicum	19050								

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium			P973					
Corynebacterium	nitrilophilus	21419					11594		
Corynebacterium	spec.			P4445					
Corynebacterium	spec.			P4446					
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090								
Corynebacterium	spec.	15954							20145	
Corynebacterium	spec.	21857								
Corynebacterium	spec.	21862								
Corynebacterium	spec.	21863								

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

TABLE 4: ALIGNMENT RESULTS

<u>ID #</u>	<u>length</u> (NT)	<u>Genbank Hit</u>	<u>Length</u>	<u>Accession</u>	<u>Name of Genbank Hit</u>	<u>Source of Genbank Hit</u>	<u>% homology</u> (GAP)	<u>Date of</u> <u>Deposit</u>
ra00062	1521	GB_HTG2:AC007366	185001	AC007366	Homo sapiens clone NH0501G22. *** SEQUENCING IN PROGRESS ***. 3 unordered pieces.	Homo sapiens	39.080	5-Jun-99
ra00084	948	GB_PR3:HSU80741 GB_PL1:BNDA1RNA GB_PR3:HSU80741 GB_GSS9:AQ163721	912 1732 912 388	U80741 X89901 U80741 AQ163721	Homo sapiens CAGH44 mRNA, partial cds. B. nigra DNA for rRNA like gene. Homo sapiens CAGH44 mRNA, partial cds. HS_2245_A1_F07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2245 Col=13 Row=K, genomic survey sequence.	Homo sapiens Brassica nigra Homo sapiens Homo sapiens	39.264 36.725 38.957 45.066	18-DEC-1997 6-Feb-97 18-DEC-1997 16-OCT-1998
ra00109	735	GB_HTG4:AC007054	171979	AC007054	Drosophila melanogaster chromosome 2 clone BACR45018 (D527) RPCH:98.45.O.18 map 41E-41E strain y; cn bw sp. *** SEQUENCING IN PROGRESS***. 13 unordered pieces.	Drosophila melanogaster	36.589	13-OCT-1998
ra00215	1449	GB_HTG4:AC007054 GB_BA1:SC9C7 GB_BA1:SC9E94 GB_BA2:AF110185	171979 31360 38532 20302	AC007054 AL035161 AL049628 AF110185	Drosophila melanogaster chromosome 2 clone BACR45018 (D527) RPCH:98.45.O.18 map 41E-41E strain y; cn bw sp. *** SEQUENCING IN PROGRESS***. 13 unordered pieces. Streptomyces coelicolor cosmid 9C7. Streptomyces coelicolor cosmid E94. Burkholderia pseudomallei strain 1026b Dbhb (dbhb), general secretory pathway protein D (gspD), general secretory pathway protein E (gspE), general secretory pathway protein F (gspF), GspC (gspC), general secretory pathway protein G (gspG), general secretory pathway protein H (gspH), general secretory pathway protein I (gspI), general secretory pathway protein J (gspJ), general secretory pathway protein K (gspK), general secretory pathway protein L (gspL), general secretory pathway protein M (gspM), and general secretory pathway protein N (gspN) genes, complete cds, and unknown genes.	Drosophila melanogaster Streptomyces coelicolor Streptomyces coelicolor Burkholderia pseudomallei	36.589 44.444 36.313 44.159	13-OCT-1998 12-Jan-99 12-Apr-99 2-Aug-99
ra00289	1299	GB_EST6:N80167	384	N80167	za65g02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:297458 Homo sapiens 3' mRNA sequence.	Homo sapiens	40.420	29-MAR-1996
ra00404	2439	GB_STS:G37084 GB_STS:G37084 GB_BA1:MTCY22D7	384 384 31859	G37084 G37084 Z83866	SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site. SHGC-56832 Human Homo sapiens STS genomic, sequence tagged site. Mycobacterium tuberculosis H37Rv complete genome, segment 133/162.	Homo sapiens Homo sapiens Mycobacterium tuberculosis	40.420 40.420 60.271	30-MAR-1998 30-MAR-1998 17-Jun-98
ra00479	2313	GB_BA1:ECU82598 GB_BA2:AE000165 GB_BA1:SCF43A	136742 12003 35437	U82598 AE000165 AL098637	Escherichia coli genomic sequence of minutes 9 to 12. Escherichia coli K-12 MG1655 section 55 of 400 of the complete genome. Streptomyces coelicolor cosmid F43A.	Escherichia coli Escherichia coli Streptomyces coelicolor	54.256 54.256 36.245	15-Jan-97 12-Nov-98 13-Jul-99
ra00497	420	GB_GSS2:CNS015U4 GB_PR3:HS4494O16 GB_BA1:MTCV78 GB_BA2:AF079544	1036 50502 33818 817	AL105910 AL117328 Z77165 AF079544	Drosophila melanogaster genome survey sequence Sp6 end of BAC BACN14G08 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence. Human DNA sequence from clone 494O16 on chromosome 22, complete sequence. Mycobacterium tuberculosis H37Rv complete genome, segment 145/162. Mycobacterium avium GroESL operon, partial sequence.	Drosophila melanogaster Homo sapiens Mycobacterium tuberculosis Mycobacterium avium	37.573 36.475 40.250 64.439	26-Jul-99 23-Nov-99 17-Jun-98 16-Aug-98

TABLE 4: ALIGNMENT RESULTS

ra00575	GB_BA1:MTGROEOP	2987	X60350	M.tuberculosis groE gene for KCS and 10-kDa products.	Mycobacterium tuberculosis 62,857	23-Apr-92
ra00599 510	GB_GSS10:AQ199703	439	AQ199703	RPC11-46013.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-46013, genomic survey sequence.	Homo sapiens 42,657	20-Apr-99
	GB_PRR2:AC002127	144165	AC002127	Human BAC clone RG305H12 from 7q21, complete sequence.	Homo sapiens 37,052	27-MAY-1997
	GB_STS:G51234	439	G51234	SHGC-80708 Human Homo sapiens STS genomic, sequence tagged site.	Homo sapiens 42,657	25-Jun-99
ra00600 1221	GB_BA1:MTCY441	35187	Z80225	Mycobacterium tuberculosis H37Rv complete genome; segment 118/162.	Mycobacterium tuberculosis 56,163	18-Jun-98
	GB_BA1:MSGY223	42061	AD000019	Mycobacterium tuberculosis sequence from clone y223.	Mycobacterium tuberculosis 37,217	10-DEC-1996
ra00605 1603	GB_BA1:BSUB0014	213420	Z99117	Bacillus subtilis complete genome (section 14 of 21): from 2599451 to 2812870.	Bacillus subtilis 36,553	26-Nov-97
	GB_BA2:AF069070	2776	AF069070	Endosymbiont of Onchocerca volvulus catalase gene, complete cds.	endosymbiont of Onchocerca volvulus 55,396	25-Nov-98
	GB_BA1:OVCAT	1845	X82176	Onchocerca volvulus endobacterial mRNA for catalase.	endosymbiont of Onchocerca volvulus 55,396	26-Nov-98
ra00648 1533	GB_BA1:SC2G5	38404	AL035478	Streptomyces coelicolor cosmid 2G5.	Streptomyces coelicolor 39,530	11-Jun-99
	GB_HTG1:HST4O16	169401	AL110119	Homo sapiens chromosome 21 clone RPC1P704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens 36,327	27-Aug-99
	GB_HTG1:HST4O16	169401	AL110119	Homo sapiens chromosome 21 clone RPC1P704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens 36,327	27-Aug-99
	GB_HTG1:HST4O16	169401	AL110119	Homo sapiens chromosome 21 clone RPC1P704O1674 map 21q21, *** SEQUENCING IN PROGRESS *** in unordered pieces.	Homo sapiens 36,327	27-Aug-99
ra00764 1239	GB_EST36:A1898007	609	A1898007	EST267450 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED31K22, mRNA sequence.	Lycopersicon esculentum 34,323	27-Jul-99
	GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YalE (yalE), LeuB (leuB), Asd (asd), FimV (fimV), and Hist (hisT) genes, complete cds; TrpF (trpF) gene, partial cds, and unknown gene.	Pseudomonas aeruginosa 35,895	23-Jun-98
	GB_BA2:PAU93274	8008	U93274	Pseudomonas aeruginosa YalE (yalE), LeuB (leuB), Asd (asd), FimV (fimV), and Hist (hisT) genes, complete cds; TrpF (trpF) gene, partial cds, and unknown gene.	Pseudomonas aeruginosa 41,417	23-Jun-98
ra00803 1353	GB_IN2:CELH34C03	27748	AF100662	Caenorhabditis elegans cosmid H34C03.	Caenorhabditis elegans 34,152	28-OCT-1998
	GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens 37,472	24-Jun-99
	GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS *** 33 unordered pieces.	Homo sapiens 37,472	24-Jun-99
ra00810 324	GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis 34,615	17-Jun-98
	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae 34,615	27-Aug-99
	GB_BA1:ECOUW76	225419	U00039	E. coli chromosomal region from 76.0 to 81.5 minutes.	Escherichia coli 52,997	7-Nov-96
ra00829 2463	GB_BA1:SC5C7	41906	AL031515	Streptomyces coelicolor cosmid 5C7.	Streptomyces coelicolor 65,269	7-Sep-98
	GB_BA1:SC5F2A	40105	AL048587	Streptomyces coelicolor cosmid 5F2A.	Streptomyces coelicolor 37,490	24-MAY-1999
	GB_BA1:STMIDRC	3374	L76359	Streptomyces peucetius daunorubicin resistance protein (drc) gene, complete cds.	Streptomyces peucetius 55,279	24-DEC-1996
ra00843 468	GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis 40,000	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

	GB_BA1:MTCY9C4	15916	Z77250	Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.	Mycobacterium tuberculosis 37.773	17-Jun-98
ra00858	568	GB_BA1:SCC54	30753	AL035591	Streptomyces coelicolor cosmid C54.	11-Jun-99
		GB_EST18:N96610	547	N96610	21286 Lambda-PRL1 Arabidopsis thaliana cDNA clone F10G317. mRNA sequence.	5-Jan-98
		GB_EST18:T45493	436	T45493	8756 Lambda-PRL2 Arabidopsis thaliana cDNA clone 133C1417. mRNA sequence.	4-Aug-98
ra00886	1269	GB_BA1:SYCSLLH	132106	D64006	Synechocystis sp. PCC6803 complete genome. 25/27. 3138604-3270709.	13-Feb-99
		GB_BA1:SCDNAJ	5611	X77458	S. coelicolor dnaK, gfpE and dnaJ genes.	21-Nov-96
		GB_BA1:STMDNAK	4648	L46700	Streptomyces coelicolor (strain A3(2)) dnaK operon encoding molecular chaperones (dnaK, dnaJ, gfpE and hspR genes, complete cds).	22-Nov-96
ra00900	975	GB_BA2:ECOUW67_0	110000	U18897	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	U18897
		GB_BA2:ECOUW67_0	110000	U18897	Escherichia coli K-12 chromosomal region from 67.4 to 76.0 minutes.	U18897
		GB_BA2:AE000393	10516	AE000393	Escherichia coli K-12 MG1655 section 283 of 400 of the complete genome.	12-Nov-98
ra00901	537	GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18. *** SEQUENCING IN PROGRESS ***. 20 unordered pieces.	22-Sep-99
		GB_HTG3:AC010757	175571	AC010757	Homo sapiens chromosome 18 clone 128_C_18 map 18. *** SEQUENCING IN PROGRESS ***. 20 unordered pieces.	22-Sep-99
		GB_HTG3:AC011283	87295	AC011283	Homo sapiens chromosome 18 clone 128_C_18 map 18. *** SEQUENCING IN PROGRESS ***. 20 unordered pieces.	07-OCT-1999
ra00981	753	GB_OV:GGA245664	512	AJ245664	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	28-Sep-99
		GB_PL2:AC007887	159434	AC007887	Gallus gallus partial mRNA for ATP-citrate lyase (ACL gene).	04-OCT-1999
		GB_GSS1:CNS00RNV	542	AL087338	Arabidopsis thaliana genome survey sequence T7 end of BAC F14D7 of IGF library from Arabidopsis thaliana strain Columbia of Arabidopsis thaliana, genomic survey sequence.	28-Jun-99
ra00995	864	GB_EST29:A1553951	450	A1553951	te54d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090497 3' similar to gb:X02067 H.sapiens mRNA for 7SL RNA pseudogene (HUMAN).; mRNA sequence.	13-Apr-99
		GB_PR3:AC003029	139166	AC003029	Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.	17-Sep-98
ra00996	864	GB_BA1:EA0014603	4479	Y14603	Erwinia amylovora srfA, srfE, srfB, srfD, srfM and srfR genes.	6-Jan-98
		GB_BA2:AE001001	10730	AE001001	Archaeoglobus fulgidus section 106 of 172 of the complete genome.	15-DEC-1997
		GB_EST30:AV018764	242	AV018764	AV018764 Mus musculus 18-day embryo C57BL/6J Mus musculus cDNA clone 1190006M16, mRNA sequence.	28-Aug-99
		GB_GSS3:B24189	377	B24189	F19E16TF IGF Arabidopsis thaliana genomic clone F19E16, genomic survey sequence. Arabidopsis thaliana	10-OCT-1997
ra01010	1242	GB_OV:AF007068	356	AF007068	Coturnix coturnix arylalkylamine N-acetyltransferase mRNA, partial cds.	12-Jul-97
		GB_EST10:AA166324	514	AA166324	ms50c09.r1 Lile Tech mouse embryo 13 5bpc 10666014 Mus musculus cDNA clone IMAGE:614992 5' similar to SWNEST_RAT P21263 NESTIN.1; mRNA sequence.	19-DEC-1996
		GB_EST7:W89968	46	W89968	mt64g11.r1 Soares mouse embryo NB/E13.5 14.5 Mus musculus cDNA clone IMAGE:419108 5' similar to SWNEST_RAT P21263 NESTIN.1; mRNA sequence.	12-Sep-96
ra01051	732	GB_GSS12:AQ381423	579	AQ381423	RPC11-135F10.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-135F10, genomic survey sequence.	21-MAY-1999
		GB_HTG6:AC010901	206121	AC010901	Homo sapiens clone RP11-544J22, WORKING DRAFT SEQUENCE. 1 unordered pieces.	04-DEC-1999

TABLE 4: ALIGNMENT RESULTS

rsa01052	432	GB_JIN1:CELC13D9	43487	AF016420	Caenorhabditis elegans cosmid C13D9.	Caenorhabditis elegans	39,344	2-Aug-97
rsa01053	543	GB_OV:CHKMAFG1	1316	D28601	Chicken novel mat-related gene matG encoding bZip nuclear protein MatG, promoter region and exon 1.	Gallus gallus	39,205	7-Feb-99
rsa01054	612	GB_PL1:PHNPNGLP	962	D45425	Pharbitis nil mRNA for Pharbitis nil Germi-like protein precursor, complete cds.	Ipomoea nil	42,925	10-Feb-99
rsa01217	723	GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	35,794	08-OCT-1999
rsa01320	1770	GB_BA2:AF031037	1472	AF031037	Neisseria meningitidis chloramphenicol acetyltransferase gene, complete cds.	Neisseria meningitidis	35,014	21-Apr-98
rsa01345	1575	GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	38,195	14-Aug-98
rsa01407	1014	GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
rsa01408	324	GB_PR4:AF152365	246546	AF152365	Homo sapiens constitutive fragile region FRA3B sequence.	Homo sapiens	41,234	1-Aug-99
rs01524	1566	GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	38,201	26-Nov-97
		GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPC1:98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPC1:98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
		GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.	Homo sapiens	32,961	07-DEC-1999
		GB_HTG6:AC010765	146468	AC010765	Homo sapiens clone RP11-115N6, *** SEQUENCING IN PROGRESS ***, 26 unordered pieces.	Homo sapiens	38,476	07-DEC-1999
		GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
		GB_HTG2:HSJ402N21	170302	AL049553	Homo sapiens chromosome 6 clone RP3-402N21 map p21.1-21.31, ***SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	36,825	03-DEC-1999
		GB_IN2:CELF18A12	29784	AF016688	Caenorhabditis elegans cosmid F18A12.	Caenorhabditis elegans	40,625	08-OCT-1999
		GB_RO:MUSMCFTR	6304	M60493	Mouse cystic fibrosis transmembrane conductance regulator (CFTR) mRNA, complete cds.	Mus musculus	37,793	10-Jun-94
		GB_HTG1:PFMAL13PA 80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
		GB_HTG1:PFMAL13PA 80518	AL109815	AL109815	Plasmodium falciparum chromosome 13 strain 3D7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Plasmodium falciparum	17,697	19-Aug-99
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	38,195	14-Aug-98
		GB_PR3:AC005224	166687	AC005224	Homo sapiens chromosome 17, clone hRPK.214_O_1, complete sequence.	Homo sapiens	36,611	14-Aug-98
		GB_HTG3:AC011500	1300851	AC011500	Homo sapiens chromosome 19 clone CIT978SKB_60E11, *** SEQUENCING IN PROGRESS ***, 246 unordered pieces.	Homo sapiens	36,446	AC011500
		GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
		GB_HTG3:AC010831	70233	AC010831	Homo sapiens clone 6_L_24, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,764	23-Sep-99
		GB_PR3:AC004058	38400	AC004058	Homo sapiens chromosome 4 clone B241P19 map 4q25, complete sequence.	Homo sapiens	40,778	30-Sep-98
		GB_PR4:AF152365	246546	AF152365	Homo sapiens constitutive fragile region FRA3B sequence.	Homo sapiens	41,234	1-Aug-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPC1:98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPC1:98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
		GB_HTG3:AC007890	121256	AC007890	Drosophila melanogaster chromosome 3 clone BACR02G21 (D722) RPC1:98 02.G.21 map 90E-91A strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 89 unordered pieces.	Drosophila melanogaster	39,432	3-Sep-99
		GB_BA1:BSUB0015	218410	Z99118	Bacillus subtilis complete genome (section 15 of 21): from 2795131 to 3013540.	Bacillus subtilis	38,201	26-Nov-97
		GB_HTG2:AC008260	107439	AC008260	Drosophila melanogaster chromosome 2 clone BACR13J10 (D924) RPC1:98 13.J.10 map 47B-47C strain y; cn bw sp, *** SEQUENCING IN PROGRESS***, 82 unordered pieces.	Drosophila melanogaster	38,302	2-Aug-99

TABLE 4: ALIGNMENT RESULTS

ra01616	1510	GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	37,873	14-Jul-99
		GB_PR4:AF111170	148083	AF111170	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene.	Homo sapiens	40,220	14-Jul-99
		GB_BA1:AEY13732	6740	Y13732	Alcaligenes eutrophus genes for ureases, ureD1, ureD2, ureA, ureB, and ORF1, ORF2.	Ralstonia eutropha	42,960	23-Sep-97
ra01616	1605	GB_BA2:AF088857	2908	AF088857	Vogesella indigofera indigoidine biosynthesis regulatory locus, complete sequence.	Vogesella indigofera	37,626	10-Sep-99
		GB_IN1:CEMO4D8	21552	Z32682	Caenorhabditis elegans cosmid M04D8, complete sequence.	Caenorhabditis elegans	37,237	23-Nov-98
		GB_EST25:AI281910	276	AI281910	q182d04.x1 NCL_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:1961767.3, mRNA sequence.	Homo sapiens	38,406	21-DEC-1998
ra01666	1500	GB_BA1:CGU43535	2531	U43535	Corynebacterium glutamicum multidrug resistance protein (cmr) gene, complete cds.	Corynebacterium glutamicum	99,933	9-Apr-97
		GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
		GB_HTG3:AC009213	114735	AC009213	Drosophila melanogaster chromosome 3 clone BACR09F18 (D812) RPCI-98 09.F.18 map 98D-98D strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 109 unordered pieces.	Drosophila melanogaster	36,111	23-Aug-99
ra01674	1017	GB_PL1:AB017159	1859	AB017159	Daucus carota mRNA for citrate synthase, complete cds.	Daucus carota	39,537	01-MAY-1998
		GB_PR1:HUMGNOS48	23142	D26607	Homo sapiens endothelial nitric oxide synthase gene, complete cds.	Homo sapiens	36,419	13-Jul-99
		GB_HTG3:AC011234	154754	AC011234	Homo sapiens clone NH0166D23, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	36,317	04-OCT-1999
ra01873	1359	GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
		GB_HTG3:AC009450	124337	AC009450	Homo sapiens chromosome 9 clone 30_C_23 map 9, *** SEQUENCING IN PROGRESS ***; 20 unordered pieces.	Homo sapiens	35,303	22-Aug-99
ra01922	1275	GB_HTG3:AC009919	134724	AC009919	Homo sapiens clone 115_L_23, LOW-PASS SEQUENCE SAMPLING.	Homo sapiens	35,409	8-Sep-99
		GB_BA1:ECONEUC	1676	M84026	E. coli protein p7 (neu C) gene, complete cds.	Escherichia coli	35,189	26-Apr-93
		GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
		GB_HTG2:AC007853	116280	AC007853	Drosophila melanogaster chromosome 3 clone BACR03L02 (D766) RPCI-98 03.L.2 map 96B-96C strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***; 80 unordered pieces.	Drosophila melanogaster	34,365	2-Aug-99
ra01936	1395	GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***; 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
		GB_HTG4:AC010037	166249	AC010037	Drosophila melanogaster chromosome 3L/66B6 clone RPCI98-6E4, *** SEQUENCING IN PROGRESS ***; 52 unordered pieces.	Drosophila melanogaster	38,534	16-OCT-1999
ra01984	420	GB_PR4:AC005552	167228	AC005552	Homo sapiens chromosome 17, clone hRPK.212_E_8, complete sequence.	Homo sapiens	36,249	26-Nov-98
		GB_PR1:HS169C8F	245	Z57239	H. sapiens Cpg island DNA genomic Mse1 fragment, clone 169c8, forward read cpg169c8.ft1a.	Homo sapiens	45,679	18-OCT-1995
		GB_BA1:SERATTBXIS	3255	L11597	Saccharopolyspora erythraea excisionase (xis) gene, integrase (int) gene, complete cds's and attB site.	Saccharopolyspora erythraea	36,232	6-Jul-94

TABLE 4: ALIGNMENT RESULTS

rx02060	GB_EST7:W97557	267	W97557	m198609.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:422296 5', mRNA sequence.	Mus musculus	42,969	16-Jul-96
rx02087 1470	GB_PR3:AC005544 GB_PL1:ATF20B18 GB_PL2:ATT25K17	169045 104738 89904	AC005544 AL049483 AL049171	Homo sapiens chromosome 17, clone hRPK.349.A.8, complete sequence. Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project). Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project).	Homo sapiens Arabidopsis thaliana Arabidopsis thaliana	35,724 35,890 38,128	25-Sep-98 24-MAR-1999 27-Aug-99
rx02088 1338	GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3. *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
	GB_HTG3:AC008697	167932	AC008697	Homo sapiens chromosome 5 clone CIT978SKB_70D3. *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	36,662	3-Aug-99
	GB_HTG3:AC008703	213971	AC008703	Homo sapiens chromosome 5 clone CIT978SKB_76P12. *** SEQUENCING IN PROGRESS *** , 54 unordered pieces.	Homo sapiens	34,768	3-Aug-99
rx02159 636	GB_BA2:AF049897	9196	AF049897	Corynebacterium glutamicum N-acetylglutarylphosphate reductase (argC), ornithine acetyltransferase (argJ), N-acetylglutamate kinase (argB), acetylornithine transaminase (argD), ornithine carbamoyltransferase (argF), arginine repressor (argR), argininosuccinate synthase (argG), and argininosuccinate lyase (argH) genes, complete cds.	Corynebacterium glutamicum	99,843	1-Jul-98
	GB_BA2:AF031518	2045	AF031518	Corynebacterium glutamicum ornithine carbamoyltransferase (argF) gene, complete cds.Corynebacterium glutamicum	Corynebacterium glutamicum	88,679	5-Jan-99
	GB_BA2:AF041436	516	AF041436	Corynebacterium glutamicum arginine repressor (argR) gene, complete cds.	Corynebacterium glutamicum	100,000	5-Jan-99
rx02184 504	GB_BA1:BS292953 GB_EST36:A1878071	8164 593	Z92953 A1878071	B.subtilis ywsf(A,B,C) genes and tbsf(A,C,D,K,R) genes. tc57a12.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5', similar to TR.Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0. ; mRNA	Bacillus subtilis Danio rerio	38,951 36,774	24-Jun-98 21-Jul-99
	GB_EST37:A1958166	641	A1958166	sequence. tc91f01.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5', similar to TR.Q13151 Q13151 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A0. ; mRNA	Danio rerio	36,774	20-Aug-99
rx02200 1233	GB_PR3:HS4494016 GB_HTG2:AC008161	50502 158440	AL117328 AC008161	Human DNA sequence from clone 494O16 on chromosome 22, complete sequence. Mus musculus clone 182_H_5. *** SEQUENCING IN PROGRESS *** , 29 unordered pieces.	Homo sapiens Mus musculus	38,648 35,938	23-Nov-99 28-Jul-99
	GB_HTG2:AC008161	158440	AC008161	Mus musculus clone 182_H_5. *** SEQUENCING IN PROGRESS *** , 29 unordered pieces.	Mus musculus	35,938	28-Jul-99
rx02201 486	GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:50010 5', mRNA sequence.	Homo sapiens	38,267	29-Jun-95
	GB_EST4:H16949	465	H16949	ym34a11.r1 Soares infant brain 11NB Homo sapiens cDNA clone IMAGE:50010 5', mRNA sequence.	Homo sapiens	36,552	29-Jun-95
rx02202 762	GB_IN1:CELCA1A3 GB_EST33:AV080151 GB_GSS5:AQ766877	37149 236 545	U41541 AV080151 AQ766877	Caenorhabditis elegans cosmid C41A3. AV080151 Mus musculus stomach C57BL/6J adult Mus musculus cDNA clone 2210413B04. mRNA sequence. HS_2017_B2_B08_MR_CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2017 Col=16 Row=D, genomic survey sequence.	Caenorhabditis elegans Mus musculus Homo sapiens	41,678 43,348 35,568	08-DEC-1995 25-Jun-99 28-Jul-99

TABLE 4: ALIGNMENT RESULTS

ra02205	1002	GB_HTG2:AC005959	127587	AC005959	Homo sapiens, *** SEQUENCING IN PROGRESS *** , 2 ordered pieces. Homo sapiens, *** SEQUENCING IN PROGRESS *** , 2 ordered pieces.	Homo sapiens	40,310	11-Nov-98
		GB_HTG2:AC005959	127587	AC005959		Homo sapiens	40,310	11-Nov-98
		GB_IN1:BRPTUBBA	4571	M36380	B.pahangi beta-tubulin gene, complete cds.	Brugia pahangi	37,703	26-Apr-93
ra02305	975	GB_RO:MUSPAFR	1140	D50872	Mouse gene for platelet activating factor receptor, complete cds.	Mus musculus	38,420	10-Feb-99
		GB_PR3:HUMARL1A	1008	L28997	Homo sapiens ARL1 mRNA, complete cds.	Homo sapiens	42,188	13-Jan-95
		GB_BA1:MLCB2533	40245	AL035310	Mycobacterium leprae cosmid B2533.	Mycobacterium leprae	42,000	27-Aug-99
ra02431	899	GB_EST4:H35255	407	H35255	EST111890 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNCO03, mRNA sequence.	Rattus sp.	39,098	2-Apr-98
		GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Homo sapiens	39,456	23-Nov-99
		GB_HTG1:HS791K14	155318	AL035685	Homo sapiens chromosome 20 clone RP4-791K14, *** SEQUENCING IN PROGRESS *** , in unordered pieces.	Homo sapiens	39,456	23-Nov-99
ra02446	558	GB_BA2:AF036166	895	AF036166	Xanthomonas campestris organic hydroperoxide resistance protein (ohr) gene, completeXanthomonas campestris		49,369	19-MAY-1998
		GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	35,417	28-DEC-1995
		GB_EST5:N25122	620	N25122	yx19d10.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:262195 5', mRNA sequence.	Homo sapiens	37,172	28-DEC-1995
ra02541	1308	GB_BA2:DPU93358	1267	U93358	Demococcus proteolyticus 40 kDa heat shock chaperone protein (dnaJ) gene, complete Deinococcus proteolyticus		42,115	17-Jan-98
		GB_EST30:A1658096	343	A1658096	cds. lc14c09.y1 Zebrafish Washu MPMIG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2., mRNA sequence.	Danio rerio	52,059	06-MAY-1999
		GB_EST37:A1959242	545	A1959242	fd25t11.y1 Zebrafish Washu MPMIG EST Danio rerio cDNA 5' similar to SW:DNJ2_HUMAN P31689 DNAJ PROTEIN HOMOLOG 2., mRNA sequence.	Danio rerio	45,438	20-Aug-99
ra02542	777	EM_PAT:E10832	1856	E10832	DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	99,000	08-OCT-1997 (Rel. 52, Created)
		GB_EST24:Z82017	396	Z82017	SSZ82017 Porcine small intestine cDNA library Sus scrofa cDNA clone c12c06 5' similarSus scrofa		37,067	30-Apr-99
		GB_OM:CATERYTHRO 681		L10606	to eukaryotic initiation factor 4 gamma, mRNA sequence.	Felis catus	39,409	14-OCT-1993
ra02543	1977	EM_PAT:E10832	1856	E10832	Cat erythropoietin mRNA, 3' end. DNA encoding Dnak protein which is one of heat shock protein from	Corynebacterium glutamicum	97,306	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:MPHSP70	2179	X59437	M.paratuberculosis gene for 70 kD heat shock protein.	Mycobacterium avium subsp. paratuberculosis	73,404	23-Apr-92
		GB_BA1:MTY13E10	35019	Z95324	Mycobacterium tuberculosis H37Rv complete genome; segment 18/162.	Mycobacterium tuberculosis	72,028	17-Jun-98
ra02586	393	GB_IN2:AC006472	156362	AC006472	Drosophila melanogaster, chromosome 2R, region 45E1-46A2, BAC clone BACR48G21, complete sequence.	Drosophila melanogaster	37,958	30-Jan-99
		GB_HTG4:AC010020	106541	AC010020	Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCINGDrosophila melanogaster		37,333	16-OCT-1999
		GB_HTG4:AC010020	106541	AC010020	IN PROGRESS *** , 55 unordered pieces. Drosophila melanogaster chromosome 3L/66D10 clone RPC198-2613, *** SEQUENCINGDrosophila melanogaster		37,333	16-OCT-1999
ra02587	2214	GB_BA1:MLCL622	42498	Z95398	IN PROGRESS *** , 55 unordered pieces. Mycobacterium leprae cosmid L622.	Mycobacterium leprae	39,848	24-Jun-97
		GB_RO:AF074879	3316	AF074879	Rattus norvegicus testis-specific protein TSPY gene, complete cds.	Rattus norvegicus	35,830	6-Jul-99

TABLE 4: ALIGNMENT RESULTS

rx03217 331	GB_RQ:RNJ001380	2641	AJ001380	Rattus norvegicus Tspy partial genomic sequence, exons 1-6.	Rattus norvegicus	37,702	29-Jun-98
	GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	37,888	27-Aug-99
	GB_HTG2:HSJ662M14	174772	AL079336	Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS	Homo sapiens	36,420	4-Feb-00
	GB_HTG2:HSJ662M14	174772	AL079336	***, 10 unordered pieces. Homo sapiens chromosome 20 clone RP4-662M14, *** SEQUENCING IN PROGRESS ***, 10 unordered pieces.	Homo sapiens	35,962	4-Feb-00